AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows:

Please replace the first paragraph of the application with the following new paragraph:

--This application is a continuation of U.S. patent application Serial No. 09/893,512, filed June 29, 2001, now abandoned, which is a continuation of U.S. patent application Serial No. 09/170,069, filed October 13, 1998, now abandoned, ~~This regular U.S. patent application claims the benefit of~~ which claims the benefit of U.S. provisional application No. 60/061,789, filed October 14, 1997, and U.S. provisional patent application No. 60/081,958, filed April 15, 1998, the entire disclosures of all of which are relied upon and incorporated herein by reference.--

Page 4, replace the first paragraph with the following new paragraph:

--In one embodiment of the invention, a heptahelix receptor of the invention has the following ~~the~~ amino acid sequence of SEQ ID NO:2 and corresponding nucleotide sequences of SEQ ID NO:1.--

Page 7, replace the second full paragraph with the following three new paragraphs:

--Figure 1 shows the nucleotide sequence (SEQ ID NO:1) of the coding region of Lyme21-9 and the deduced amino acid sequence (SEQ ID NO:2) of the corresponding human CMKRL1 receptor.

Plasmid clone Lyme21-9 was deposited on July 11, 2002, at the American Type Culture Collection ("ATCC"), 10801 University Blvd., Manassas, VA 20110-2209, in accordance with the Budapest Treaty, and was assigned accession number PTA-4543.

The first nucleotide and amino acid residue of the translation start site are designated as position 1. The putative transmembrane segments TMI-TMVII are indicated by solid lines; the extension of each segment is estimated on the basis of the hydrophobicity profile and sequence alignment of other heptahelix receptors. Potential glycosylation sites are indicated with arrowheads.--

Page 8, replace the first paragraph with the following new paragraph:

--Figure 3 depicts the alignment of the complete amino acid sequences for eight human chemotactic receptors (SEQ ID NOs:9-16) together with the amino acid sequence deduced from the presently cloned cDNA (Lyme 21-9; SEQ ID NO:2) showing the high degree of similarity ~~(shaded areas)~~, not least within the transmembrane regions. The homology presentation was done with the SeqVu (version 1) mode in the GCG program. The scaling system used is described by Riek et al. (1995).--

Page 8, replace the last paragraph with the following new paragraph:

--Figure~~s 5A and 5B~~ 5 depicts fluorescence photomicrographs with examples of FISH mapping of the gene corresponding to CMKRL1. Fig. 5A shows fluorescent signals on one human chromosome. Fig. 5B shows the same mitotic figures stained with DAPI to identify chromosome 14. Original magnification was x1300.--

Page 10, replace the last paragraph with the following new paragraph:

--Figures 12A and 12B ~~12~~ depicts the results of fluorescence immunocytochemistry of a monoclonal antibody (mAB) raised against a synthetic peptide corresponding to the first 15 amino acid residues in the extracellular tail of CMKRL1 showing (a) finely-granular fluorescence in the periphery of CHO cells stably expressing CMKRL1, and (b) absence of fluorescence in sham-transfected control cells. Magnification: 500x.--.

Replace the paragraph bridging pages 26 and 27 with the following new paragraph:

--Sequence comparison with cloned receptors within the G-protein-linked superfamily showed most similarity with the subfamily of chemoattractant leukocyte receptors (Fig. 3), particularly the "classical" chemoattractants, C5a and *N*-formyl-methionyl-leucyl-phenylalanine (fMLP) (Fig. 4). For example, there is (in the GCG/fasta matrix score) an approximately 30% overall sequence identity with the human C5a anaphylatoxin receptor (Gerard and Gerard, 1991) and 28% identity with the fMLP receptor (Boulay *et al.*, 1990; Thomas *et al.*, 1990). Taken as a group together with the Lyme21-9 receptor cDNA clone (Fig. 3), there is a particularly high degree of consensus in the GN-LVVLV (SEQ ID NO:7) sequence motif in the TMI region and the LLNLA--DLLF--TLP-W (SEQ ID NO:8) motif within TMII.--

Replace the paragraph bridging pages 47 and 49 with the following new paragraph:

--A cDNA library of a human B-cell lymphoblast cell line (GM03299; NIGMS Human Genetic Mutant Cell Repository, Camden, NJ) was constructed from poly(A)$^+$-selected RNA in the pcD/SP6/T7 cloning and expression vector (Morel *et al.*, 1992), a derivative of Okayama-Berg's pcD vector (Okayama *et al.*, 1987). The library contained 7.5×10^6 recombinants. Plasmid preparation was prepared by cesium chloride-ethidium bromide banding (Sambrook *et al.*, 1989) and used as template (1 µg) in PCR (Mullis and Faloona, 1987) attempting to amplify a DNA stretch between the putative TMII and TMVI of G-protein-coupled receptors. The sense primer was a 27-mer oligonucleotide with 250-fold degeneracy (5'- A(T)TCCTGGTG(C)A(T)G(A)CCTT(G)GCT(A)G(T)TGG CC(T)GAC-3' (SEQ ID NO:3)); the antisense primer was a 29-mer oligonucleotide with 128-fold degeneracy (5'- AT(G)GA(T)AGA(T)AGGGCAGCCAGCAGAC(G)C(G)G(A) T(C)GAA-3' (SEQ ID NO:4)). The primers were used in 1µM concentrations together with *Taq* polymerase (Genamp; Perkin-Elmer Cetus). Forty cycles of 96°C for 45 s (denaturation), 55°C for 4 min (annealing), and 72°C for 4 min (extension) were carried out, followed by a final extension at 72°C for 15 min. The products were analyzed on a 3% NuSieve genetic technology-grade agarose gel (FMC BioProducts). Three bands between 500 and 700 bp in size were excised and blunted with T4 polymerase, and terminal phosphates were added with T4 polynucleotide kinase (New England Biolabs).

The fragments were subcloned into the *Hinc*II site of the M13mp18 vector and sequenced according to Sanger's dideoxynucleotide termination method. Several sequences exhibited homology with the G-protein-coupled superfamily. Sequence information from one insert (hLym10) was utilized to obtain a full-length cDNA clone.--

Replace the paragraph bridging pages 49 and 50 with the following new paragraph:

--On the basis of sequence stretches in the PCR clone corresponding to the putative first extracellular and third intracellular loops, two 48-bp oligonucleotides were synthesized, one designated Lym5, 5'-ACACAGGAGGCAACCAGCCAGTCCAAAA CTCCAGGTGCCTTGGGCCAG-3' (SEQ ID NO:5), and the other Lym6, 5'-GATCGGT GCCAGCACCCGCCGGGCCATCGCCTTGGTGCGTAGCTTCTG-3' (SEQ ID NO:6). They were labeled with [γ-^{32}P]ATP (5000 Ci/mmol, Amersham) and used in combination as probes to screen pools of recombinants prepared from consecutive dilutions (Bonner *et al.,* 1987) of the human B-cell lymphoblast cDNA library. Hybridization of Southern blots was performed in 3 x SSC (0.45 M NaCl, 0.05 M sodium citrate, pH 7.0) at 60°C, and the filters were washed in 1 x SSC at the same temperature. A positive band of 1.7 kb in size was followed until a single clone (designated Lyme21-9) was obtained. Overlapping restriction fragments were subcloned into M13 phage vectors for sequencing of both cDNA strands. Sequence analysis and comparisons were performed with Genetics Computer Group software (University of Wisconsin) and with GenBank as well as with the GeneWorks program from IntelliGenetics (Mountain View,

CA). Hydrophobicity tests of the deduced amino acid sequence were carried out according to Kyte and Doolittle (1982). Chromosome mapping results were evaluated in the Genome Data Base (GDB 6.0) and the NCBI database (Online Mendelian Inheritance in Man; OMIM).--